IN THE SPECIFICATION

Please add page number "1" to the first page of the disclosure.

Please replace the paragraph beginning on page 72, line 12 and ending on line 23 with the following amended paragraph:

Phagocytic and killing activity of macrophages

MDM were plated in 24-well non-tissue culture treated dishes for 10 days in 40% human serum. Cells were pre-incubated with 180 μg ml^{-1} mouse IgG (Sigma) or 180 μg ml^{-1} anti-vimentin IgG antibody (Sigma) for 12 h. The cells were then infected with 1 x 10^6 colony forming units of *E. coli* (DH5-α, Gibco-BRL, Grand Island, NY). After 1 h incubation, the wells were extensively washed to remove non-phagocytosed bacteria, and the wells in one plate were lysed with sterile 0.5% ~~Triton~~ TRITON X-100 (polyethylene glycol p-(1,1,3,3-tetramethylbutyl)-phenyl ether) for the bacterial phagocytosis assay. Fresh media was added to the other plate and this was incubated for an additional 2 h, after which the cells were lysed with 0.5% ~~Triton~~ TRITON X-100 (polyethylene glycol p-(1,1,3,3-tetramethylbutyl)-phenyl ether) for the bacterial killing assay. Serially diluted cell lysates were plated on agar (Difco, Detroit MI) and incubated overnight at 37 ^{0}C, and the number of colonies was counted. Killing rate = [1-(CFU at 3h/CFU at 1h)] x100 42.

Please replace the paragraph beginning on page 32, line 24 and ending on page 33, line 8 with the following amended paragraph:

In another screening method, secretory vimentin or a fragment of secretory vimentin, are immobilized. Polypeptides can be immobilized using methods known in the art, such as adsorption onto a plastic microtiter plate or specific binding of a GST-fusion protein to a polymeric bead containing glutathione. For example, GST-vimentin is bound to ~~glutathione-Sepharose~~ glutathione-SEPHAROSE (agarose polysaccarhide polymer) beads. The immobilized peptide is then contacted with another peptide with which it is capable of binding in the presence and absence of a candidate compound.

Unbound peptide is then removed and the complex solubilized and analyzed to determine the amount of bound labeled peptide. A decrease in binding is an indication that the candidate compound inhibits the interaction of vimentin with the other peptide. A variation of this method allows for the screening of compounds that are capable of disrupting a previously formed protein/protein complex. For example, in some embodiments a complex comprising vimentin or a vimentin fragment bound to another peptide is immobilized as described above and contacted with a candidate compound. The dissolution of the complex by the candidate compound correlates with the ability of the compound to disrupt or inhibit the interaction between vimentin and the other peptide.

Please replace Table I of the published application (No.: 20040121419) with the following amended Table I.

1TABLE I Isolation and Partial Amino Acid Sequence Analysis of Vimentin from the Supernatant of MDM* 1 mstrsvssss yrrmfggpgt asrpsssrsy vttstrtysl gsalrpstsr slyasspggv 61 yatrssavrl rssvpgvrll qdsvdfslad aintefkntr tnekvelqel ndrfanyidk 121 vrfleqqnki llaeleqlkg qgksrlgdly eeemrelrrq vdqltndkar veverdnla 181 dimrlreklq eemlqreeae ntlqsfrqdv dnaslarldl erkveslqee iaflkklhee 241 eiqelqaqiq eqhvqidvdv skpdltaalr dvrqqyesva aknlqeaeew ykskfadls 301 aanrnndalr qakqesteyr rqvqsltcev dalkgtnesl erqmremeen faveaanyqd 361 tigrlqdeiq nmkeemarhl reyqdllnvk maldieiaty rkllegeesr islplpnfss 421 lnlretnlds lplvdthskr tlliktvetr dgqvinetsq hhddle *Amino acid stretches identified as identical to vimentin during protein sequence analysis are underlined. Sequence analysis was performed at the Harvard Microchemistry Facility by microcapillary reverse-phase HPLC nano-electrospray tandem mass spectrometry (.mu.LC/MS/MS) on a Finningan LCQ quadrupole ion trap mass spectrometer. SEQ ID NO:1 refers to the full length vimentin sequence of amino acids 1 to 466. SEQ ID NO:2 refers to amino acids 105 to 113. SEQ ID NO:3 refers to amino acids 130 to 140. SEQ ID NO:4 refers to amino acids 160 to 170. SEQ ID NO:5 refers to amino acids 295 to 304. SEQ ID NO:6 refers to amino acids 346 to 373. SEQ ID NO:7 refers to amino acids 411 to 420. SEQ ID NO:8 refers to amino acids 425 to 439.